SEQUENCE LISTING

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<110> Ling, Nicholas
      Gaur, Amitabh
      Conlon, Paul J.
      Steinman, Lawrence

<120> METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
      USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
      PROTEIN

<130> 690068.405C3

<140> US 10/015,546
<141> 2001-12-11

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(513)

<400> 1
gcg tca cag aag aga ccc tcc cag agg cac gga tcc aag tac ctg gcc    48
Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
 1               5                  10                  15

[illegible]    96
Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
[illegible]

[illegible]    144
Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
[illegible]

[illegible]    192
Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala
[illegible]
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cgc aca cca ccc ccg tcg cag gga aag ggg aga gga ctg tcc ctg agc     336
Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
            100                 105                 110

aga ttt agc tgg ggg gcc gaa ggc cag aga cca gga ttt ggc tac gga     384
Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
        115                 120                 125

ggc aga gcg tcc gac tat aaa tcg gct cac aag gga ttc aag gga gtc     432
Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val
    130                 135                 140

gat gcc cag ggc acg ctt tcc aaa att ttt aag ctg gga gga aga gat     480
Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp
145                 150                 155                 160

agt cgc tct gga tca ccc atg gct aga cgc tga                         513
Ser Arg Ser Gly Ser Pro Met Ala Arg Arg  *
                165                 170


<210> 2
<211> 170
<212> PRT
<213> Homo sapiens

<400> 2
Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
1               5                   10                  15
Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
            20                  25                  30
Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
        35                  40                  45
Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala
Arg Thr Ala His Tyr Gly Ser [illegible] [illegible] [illegible] Lys Ser His Gly Arg Thr
[illegible]
Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
            100                 105                 110
Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
        115                 120                 125
Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val
    130                 135                 140
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(516)

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Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
 1   5   10   15

gcc aca gca agt acc atg gac cat gcc agg cat ggc ttc ctc cca agg 96
Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
            20   25   30

cac aga gac acg ggc atc ctt gac tcc atc ggg cgc ttc ttt ggc ggt 144
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
        35   40   45

gac agg ggt gcg cca aag cgg ggc tct ggc aag gac tca cac cac acc 192
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Thr
    50   55   60

[illegible] 240

[illegible] 288

[illegible] 336

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gtc gat gct gaa ggt act ctt tct gga tca ccc atg gct aga agg tga
Val Asp Ala Glu Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
145                 150                 155                 160

gat agt cgc tct ggg tca ccc atg gct aga agg tga
Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg  *
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<211> 171
<212> PRT
<213> Homo sapiens

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Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
 1               5                  10                  15
Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
            20                  25                  30
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
        35                  40                  45
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
    50                  55                  60
Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
65                  70                  75                  80
Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr
                85                  90                  95
Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu
            100                 105                 110
Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr
        115                 120                 125
Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly
    130                 135                 140
Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
145                 150                 155                 160
Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
                165                 170
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